

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 28, 2002, 17:31:09 ; Search time 63.43 Seconds
(without alignments)
613.651 Million cell updates/sec

Title: US-09-502-984B-1
Perfect score: 1194
Sequence: 1 APPPNLPDPKFKSKALIAA.....GGFWSAMSEPPSILTPSDLD 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1005.5	84.2	509	6 Q9MYZ9	Q9MYZ9 sus scrofa
2	965.5	80.9	316	11 O35545	O35545 rattus norv
3	851	71.3	229	6 Q27950	Q27950 bos indicus
4	846	70.9	229	6 Q28206	Q28206 bos taurus
5	778.5	65.2	387	6 Q95N13	Q95N13 ovis aries
6	778.5	65.2	418	6 Q95N14	Q95N14 ovis aries
7	185	15.5	566	11 Q925F5	Q925F5 mus musculu
8	160.5	13.4	422	4 Q75462	Q75462 homo sapien
9	159.5	13.4	422	4 Q9UHH5	Q9UHH5 homo sapien
10	159	13.3	296	6 O18880	O18880 bos taurus
11	157.5	13.2	425	11 Q9JMS8	Q9JMS8 mus musculu
12	151	12.6	581	6 O46561	O46561 ovis aries
13	140.5	11.8	626	13 Q90WG7	Q90WG7 cynops pyrr
14	140	11.7	227	6 Q9GLM3	Q9GLM3 ursus marit
15	139	11.6	625	6 Q9XS92	Q9XS92 trichosurus
16	137	11.5	622	6 Q9N0J7	Q9N0J7 callithrix

17	128	10.7	288	4 Q96P36	Q96P36 homo sapien
18	128	10.7	349	4 Q9UH35	Q9UH35 homo sapien
19	128	10.7	376	4 Q96P35	Q96P35 homo sapien
20	126	10.6	521	4 Q96TF0	Q96TF0 homo sapien
21	126	10.6	608	11 Q99JZ1	Q99JZ1 mus musculu
22	124.5	10.4	611	13 Q9PTI9	Q9PTI9 xenopus lae
23	123.5	10.3	636	13 Q90Z16	Q90Z16 parallithy
24	123.5	10.3	1093	11 Q70535	Q70535 rattus norv
25	122.5	10.3	634	6 Q46600	Q46600 bos taurus
26	122	10.2	206	4 Q16354	Q16354 homo sapien
27	122	10.2	346	13 Q93404	Q93404 oreochromis
28	120.5	10.1	638	6 Q95JF2	Q95JF2 allutropoda
29	118.5	9.9	538	13 Q9DFU0	Q9DFU0 sparus aura
30	114.5	9.6	608	6 Q9N0Y7	Q9N0Y7 monodelphis
31	113.5	9.5	4280	5 Q9UBZ9	Q9UBZ9 caenorhabdi
32	113.5	9.5	4450	5 Q9UBZ8	Q9UBZ8 caenorhabdi
33	112.5	9.4	638	6 Q9TU69	Q9TU69 canis famli
34	111.5	9.3	611	13 Q91BF6	Q91BF6 xenopus lae
35	111.5	9.3	611	13 Q9PTI0	Q9PTI0 xenopus lae
36	111	9.3	198	6 Q18985	Q18985 cervus elap
37	110.5	9.3	632	6 Q95ML5	Q95ML5 salmatri bol
38	109	9.1	600	13 Q9PTP0	Q9PTP0 carassius a
39	108.5	9.1	467	11 Q63216	Q63216 rattus norv
40	107.5	9.0	615	13 Q9DB35	Q9DB35 pelodiscus
41	107.5	9.0	628	11 Q9JKT1	Q9JKT1 cavia porce
42	107.5	9.0	628	11 Q9JKT1	Q9JKT1 cavia porce
43	107.5	9.0	628	11 Q9J197	Q9J197 cavia porce
44	106.5	8.9	229	4 Q14213	Q14213 homo sapien
45	106.5	8.9	390	4 Q9UEH7	Q9UEH7 homo sapien

ALIGNMENTS

RESULT 1
Q9MYZ9 PRELIMINARY; PRT; 509 AA.
ID Q9MYZ9;
AC Q9MYZ9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ERYTHROPOIETIN RECEPTOR.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,
Christenson R.K., Vallet J.L.;
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in
Embryonic and Fetal Liver."
RT Domest. Anim. Endocrinol. 0:0-0(2000).
DR EMBL; AF274305; AAF77065.1; -.
DR HSSP; P19235; 1BBA.
DR InterPro: IPR002996; CRA.
DR InterPro: IPR000572; Euk_cxidored_molylb.
DR InterPro: IPR003861; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_FL.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_FL; UNKNOWN_1.
DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCDB8 CRC64;

Query Match 84.2%; Score 1005.5; DB 6; Length 509;
Best Local Similarity 84.5%; Pred. No. 1.6e-86;
Matches 191; Conservative 9; Mismatches 25; Indels 1; Gaps 1;
QY 1 APPPNLPDPKFKSKALIAARGPETLCTFRLDLVCFWEASAGVGPNYSFYLE 60

Db	25	APSPNSPAKFFSSKALLLAARGPEELCTTERLELDJVCWEAGSAGVCPEDYSSTOLE	84
Qy	61	DEPKLCLRLHQAPTARGAVFCWCSLPTADTSFVPLELRVT--AAGCAPYHRYIHINEVY	119
Db	85	GPMPKCHLHOGPTARGSVFMCSLPTADTSFVPLELRVTEVSSGAPYHRIIHINEVY	144
Qy	120	LDDAVGVGLARLADSSGHVVLRLMPPPEPMTSHIRYEDVSGANGAGSVORVEILEGRT	179
Db	145	LDDPAGGLIARAEESSGHVVLRLMPPPPGAPMAMSLIRYEVNISTENRAGGVORVEIILDGRT	204
Qy	180	ECVLSNLGRGRTYRTPAVRARMAEPSPGFGWASMSSEPVSLLRPSDD	225
Db	205	ECVLSNLGRGRTYRTPFVVRARMAEPSPGGFWASMSSEPSALLTRASDD	250
RESULT	2		
ID	035545	PRELIMINARY;	PRT; 316 AA.
AC	035545;		
DT	01-JAN-1998	(TREMBLrel. 05, Created)	
DT	01-JAN-1998	(TREMBLrel. 05, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	INTRON 5-INSERTED FORM OF ERYTHROPOIETIN RECEPTOR PRECURSOR.		
OS	Rattus norvegicus (rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_Taxid=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98296111; PubMed=9630610;		
RA	Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,		
RA	Miyatake K., Nakano Y.;		
RT	"Type I intron 5-inserted form of rat erythropoietin receptor is		
RT	expressed as a membrane-bound form."		
RL	Biochim. Biophys. Acta 1403:169-178(1998).		
DR	EMBL; D83509; BAA22373.1; -.		
DR	HSSP; P19235; 1EBA.		
DR	InterPro; IPR002996; CRIA.		
DR	InterPro; IPR003961; FN.III.		
DR	InterPro; IPR003528; Hematopo_receptor_IL_F1.		
DR	Pfam; PF00041; fn3.1.		
DR	SMART; SM00060; FN3.1.		
DR	PROSITE; PS01352; HEMATOPO_REC_IL_F1; UNKNOWN_1.		
KW	Signal; Receptor.		
FT	SIGNAL	1	24
FT	CHAIN	25	316
FT	SEQUENCE	316 AA; 34220 MW; 05044BF8516C180B CRC64;	POTENTIAL.

[illegible]

ID	Q27950	PRELIMINARY;	PT:	229 AA.
AC	Q27950:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ERYTHROPOIETIN RECEPTOR (FRAGMENT).			
GN	EPOR.			
OS	Bos indicus (Zebu).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OX	Bovidae; Bovinae; Bos.			
OX	NCBI_taxid=9915;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BONE MARROW;			
RA	Suliman H.B., Feldman B.F., Majima P.A.O., Logan-Hentley L.L.;			
RL	Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; U61398; AAB03870.1; -.			
DR	HSSP; P19235; 1EBA.			
DR	InterPro; IPR002996; CRA.			
DR	InterPro; IPR003961; FN.III.			
DR	InterPro; IPR003528; Hematopo_receptor_L.F1.			
DR	Pfam; PF00041; In3; 1.			
DR	SMART; SM00060; FN3; 1.			
DR	PROSITE; PS01352; HEMATOPO_REC_L.F1; UNKNOWN_1.			
KM	Receptor.			
ET	NON_TER	1	1	
ET	NON_TER	229	229	
SO	SEQUENCE	229 AA;	25196 MW;	FEEDIC4AB07893E8 CMC64;

Query Match Similarity	71.3%	Score 851	DB 6	Length 229
Best Local Similarity	84.3%	Pred. No. 2,2e-72		
Matches 161	Conservative	6	Mismatches 24	Indels 0
				Gaps 0
Qy	35	DLVCFWEEDASAGVPGNGSYFSLQLEDEPWKLCRLHQAPTAGAVRFMCSLPTADTSSFV	94	
Db	1	DLVCFWEEDAAATAGVPGDPNYSFYSLQLEGEPMKRCRLHQAPTAGLVRFMCSLPTADTSSFV	60	
Qy	95	PLELHVTAASGAPRHYRIHNEVYLLDAPGLVARLDESGHYVLRMLPPPEPMTSHI	154	
Db	61	PLELHVTAASGASRRIRTIHNEVYLLDPPARLVARRDDEGHVYLRMLPPGAMASLI	120	
Qy	155	RYEVDVSAGNGASQVQRIELLEGTECVLSNLGRTRYTFAVRARMAPSPFGGFSAMSE	214	
Db	121	RYEVNISAEENAGSAQRIEILDGRTECLSLNLGRGTRTFYFVARMAPSPFGGFSAMSE	180	
Qy	215	PYSLLTPSDLD	225	
Db	181	PASLLTPASDLD	191	
RESULT	4			
Q28206				
ID	Q28206	PRELIMINARY	PRT	229 AA.
AC	Q28206			
DT	01-NOV-1996	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)		
DE	ERYTHROPOIETIN RECEPTOR (FRAGMENT).			
GN	EPOR.			
OS	Bos taurus (Bovine).			
OC	Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
OX	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=NONE MARROW;			
RA	Suliman H.B., Feldman B.F., Majima P.A.O., Logan-Henfrey L.L.;			
RL	Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; U61399; AAB03871.1; -.			
DR	HSSP; P19235; IERA.			

SEQUENCE 566 AA; 63339 MW; A19D3DD5F7BDBA6B CRC64;

Query Match 15.5%; Score 185; DB 11; Length 566;

Best Local Similarity 27.0%; Pred. No. 4.1e-09; Mismatches 100; Indels 42; Gaps 7;

Db 13 SKAALLAARGPEELICFTEERLEDVCFWEBAASAGVPGNYSFYOLEDEPMKLCRLHQA 72
 18 SQDVFLLALGCTEPLNCFSCFFEDLTCFWEDEEAA--PSGYQLLYAVRGKPRACPLYSQ 75
 QY 73 PIARGAVRENCISLPTAD-TSSFVPLELRYTAAS-GAPRHRVYHT-----NE 117
 Db 76 SVPTFGTRVYQCPADDEVAFLEFPLHLWKVNSLNOTLIDRVLFVSVETCPTLMMPNP 135
 QY 118 VYLLDAPVGVVARLADSGHVLRWLPPPETMTHIRYFVDVSAGNAGSVQVRELLEG 177
 Db 136 VPLDPPCPVHPASQPHGV--RTSPAGAPF-----LTKGGS-----173
 QY 178 RTECVSLNLGRTRYTFVAVRARMAPSPFGGFWASMESEPSLTPSD 223
 Db 174 ---CLVSGIQAGKSYMLQLRSQPDGVSLRSGWGPMSPPVVDLPD 216

RESULT 8
 ID 075462 PRELIMINARY; PRT; 422 AA.
 AC 075462;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CYTOKINE-LIKE FACTOR-1 PRECURSOR.
 GN CLF-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
 RA Menoud L.N., Wells T.N.C., Kosco-Villbols M.H., Gauchat J.F.,
 RT CLF-1, a Novel Soluble Protein Shares Homology With Members of the
 RT Cytokine Type-1 Receptor Family.";
 RL J. Immunol. 0:0-0(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Magrangeas F., Jacques Y., Minvielle S.,
 RT Cloning and expression of a novel soluble protein containing
 RT hematopoietic cytokine receptor domains.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF059293; AAC2835.1;
 DR EMBL: AF073515; AAD39681.1;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 KW Signal; Receptor.
 FT SIGNAL 1 37
 FT CHAIN 38 422 POTENTIAL.
 FT SEQUENCE 422 AA; 46301 MW; AD9DEFCB01B84228 CRC64;

Query Match 13.4%; Score 160.5; DB 4; Length 422;
 Best Local Similarity 26.3%; Pred. No. 5.8e-07;
 Matches 60; Conservative 29; Mismatches 84; Indels 55; Gaps 13;

QY 23 PEBLCTFERLEDVCFWEBAASAGVPG-----NYSFSYOLEDEPW---KLCRL 69
 Db 138 PVNISCKMKMKDLTCMT-----PGAHGTFPLHTNLSLKYKLR---WYGQDNICEE 166
 QY 70 HQAPTRAGAVRFWCSLPTADTSSFVPLELRYTAAS--GAPRHR-VYIHINEVYLLDAPVG 126

Db 187 YHTVGPHS-----CHIP-KDLALFTPEIWEATNRLSARSQVLTLDLVDVTTDPPD 240
 QY 127 L-VARLADESGHYVLRWLPPPET-----PMTSHIREYVDVSAGNAGSVQVREILLEGRT 180
 Db 241 VHSKRVGGLLEDQLSVRWSPFPALKDFLFOAKYQIRRVEDSV-----DKKVVDDVSNQIS 295
 QY 181 CVLSNLGRTRYTFVAVRARMAPSPFG-----GFWASMESEPSLTP 221
 Db 296 CRLAGLKPQTVYFVQVRCN----PFGYGSKKAGIWESEMSHPTAATP 339

RESULT 9
 ID 090HH5 PRELIMINARY; PRT; 422 AA.
 AC 090HH5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CLASS I CYTOKINE RECEPTOR.
 GN ZCYTORS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lok S., Presnell S.R., Jellmeberg A.C., Gilbert T., Whitmore T.E.,
 RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF178684; AAD54385.1;
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR Pfam: PF00041; fn3; 2.
 DR SMART: SM00060; FN3; 2.
 KW Receptor.
 SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 13.4%; Score 159.5; DB 4; Length 422;
 Best Local Similarity 26.3%; Pred. No. 7.3e-07;
 Matches 60; Conservative 29; Mismatches 84; Indels 55; Gaps 13;

QY 23 PEBLCTFERLEDVCFWEBAASAGVPG-----NYSFSYOLEDEPW---KLCRL 69
 Db 138 PVNISCKMKMKDLTCMT-----PGAHGTFPLHTNLSLKYKLR---WYGQDNICEE 186
 QY 70 HQAPTRAGAVRFWCSLPTADTSSFVPLELRYTAAS--GAPRHR-VYIHINEVYLLDAPVG 126
 Db 187 YHTVGPHS-----CHIP-KDLALFTPEIWEATNRLSARSQVLTLDLVDVTTDPPD 240
 QY 127 L-VARLADESGHYVLRWLPPPET-----PMTSHIREYVDVSAGNAGSVQVREILLEGRT 180
 Db 241 VHSKRVGGLLEDQLSVRWSPFPALKDFLFOAKYQIRRVEDSV-----DKKVVDDVSNQIS 295
 QY 181 CVLSNLGRTRYTFVAVRARMAPSPFG-----GFWASMESEPSLTP 221
 Db 296 CRLAGLKPQTVYFVQVRCN----PFGYGSKKAGIWESEMSHPTAATP 339


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DR EMBL: Y10808; CAAT1766.1; -.
DR HSSP: P14787; IAN3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PR00041; fn3; 2.
DR SMART: SM00060; FN3; 2.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPLIC 24 66
FT FT
FT VARSPLIC 67 581
FT VARSPLIC 286 296
FT FT
FT VARSPLIC 297 581
FT CONFLICT 281 281
FT CONFLICT 387 387
FT SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;

Query Match
Best Local Similarity 24.4%; Score 151; DB 6; Length 581;
Matches 55; Conservative 36; Mismatches 104; Indels 30; Gaps 10;

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QY 15 AALLAARGPE---LICFTEILEDVCFWEAASAGVPGNTSFSYQLEDEPWKLCRLH 70
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 19 ASILNGOSPEKPKLIKCRSPKETFQWMEPGADGGL-PTNYTLVYRKGE---TLIH 73
QY 71 QAPTAGAVAFWCSLPTADTSSFPVLELRVTA-----ASGAPRYHVIHINEVLLDAP 124
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 74 ECPDYKGTGPNCSYFSSKKTYSIMKMYITVASINQMGISSDPLY--VDVYIVDEPP 130
QY 125 VGLVARL---ADESGHVLRLPPEPTPMTS---HIREYDVASAGNSVQHEILEGR 178
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 131 VNLTLEKHEDKRPYIMIKMSPTLIDVKSQWFSIQYELRLKPEKATD--WETHFAPKL 188
QY 179 TECVLNMLRGRTYTFVAVRARAPEPSFGFSAMSEPVSLITPSD 223
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 189 TQKIFNLYPGOKYLVQIRCK---PDH-GYWSMSESPESIQIPND 229

RESULT 13
Q90MG7 PRELIMINARY; PRT; 626 AA.
AC Q90MG7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Salamandridae; Cynops.
OX NCBL_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Yamamoto T., Nakayama Y., Matsuda Y., Abe S.-I.;
RT "Cloning and expression of a cDNA encoding a prolactin receptor of the
RT Japanese red-bellied newt, Cynops pyrrhogaster."
RL Zool. Sci. 15:741-747(1998).

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DR EMBL: AB005045; BAB61107.1; -.
KW Signal; Receptor.
FT SIGNAL 1 26
SQ SEQUENCE 626 AA; 69944 MW; B6050DD9C9F58DES CRC64;

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Query Match
Best Local Similarity 21.7%; Score 140.5; DB 13; Length 626;
Matches 47; Conservative 38; Mismatches 95; Indels 37; Gaps 8;

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QY 23 PEELFTEILEDVCFWEAASAGVPGNTSFSYQLEDEPWKLCRLHQPARGAVRFM 82
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 34 PVNIMKRSPEKETFSCWMOGSDGGL-PTNYTLVYRKGN-----TYSECPDYKTSGPS 88
QY 83 CSLPTADTSSFPVLELRVTA-----ASGAPRYHVIHINEVLLDAPVGLVARLADESG 136
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 89 CFEDKHTSIWTFWYNIIVANTELSTSDPKF--VDVAYIVQLPPLNVLSTLIEYEP 145
QY 137 HVLRLPPEPTPMTS---HIREYDVASAGN-----AGSYQVEILLEGRTECVLSN 186
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 146 HLLVKSPPSEADYKSGWYIIEYVQFKSKAKEMETLRAGKQRLKVF-----SL 196
QY 187 RGRRTFAVRARMAPEPSFGFSAMSEPVSLITPSD 223
DB 197 NPSENTIVQIRCK---SDHGFSMMSPESTYIQIPND 229

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RESULT 14
Q9GLM3 PRELIMINARY; PRT; 227 AA.
AC Q9GLM3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PROLACTIN RECEPTOR (FRAGMENT).
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBL_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA MEDLINE=20086658; PubMed=10618652;
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;
RT "Cloning and sequence analysis of the extracellular region of the
RT polar bear (Ursus maritimus) luteinizing hormone receptor (Lhr)
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor
RT (PRLr) genes and their expression in the testis of the black bear
RT (Ursus americanus)."
RL Mol. Reprod. Dev. 55:136-145(2000).
DR EMBL: AF169792; AAG10648.1; -.
DR HSSP: P14787; IAN3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR Pfam: PR00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON_TER 1 227
FT TER 227
SQ SEQUENCE 227 AA; 26114 MW; F5E6C5F3B5D5B49 CRC64;

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Query Match
Best Local Similarity 11.7%; Score 140; DB 6; Length 227;
Matches 51; Conservative 33; Mismatches 86; Indels 40; Gaps 10;
QY 34 EDLVCFWEAASAGVPGNTSFSYQLEDEPWKLCRLHQPARGAVRFWCSLPTADTSSFP 93
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 2 EFTFCWKKPEEDGGL-PTNYTLVYRKGE---TTTCECPDYISSGPNCSYFNKKHTSIW 56
QY 94 VPLELRVTA-----ASGAPRYHVIHINEVLLDAPVGLVARL---ADESGHVLRLP 144
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 57 TMTIITINATNMGSSSDPRY--VDVYIIVPDPVNLTELRKPEDKRPYLMKKWTF 113

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